

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ozenberger, Brad A.
Jacobsen, J. S.
Kajkowski, Eileen
- (ii) TITLE OF INVENTION: β -Amyloid Peptide-Binding Proteins
and Polynucleotides Encoding the Same
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: American Home Products
 - (B) STREET: One Campus Drive
 - (C) CITY: Parsippany
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07054
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Walsh, Andrea C.
 - (B) REGISTRATION NUMBER: 34,988
 - (C) REFERENCE/DOCKET NUMBER: 98126
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 973-683-2169
 - (B) TELEFAX: 973-683-4117

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 810 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: mRNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CAT ATT TTA AAA GGG TCT CCC AAT GTG ATT CCA CGG GCT CAC GGG Met His Ile Leu Lys Gly Ser Pro Asn Val Ile Pro Arg Ala His Gly	48
1 5 10 15	
CAG AAG AAC ACG CGA AGA GAC GGA ACT GGC CTC TAT CCT ATG CGA GGT Gln Lys Asn Thr Arg Arg Asp Gly Thr Gly Leu Tyr Pro Met Arg Gly	96
20 25 30	
CCC TTT AAG AAC CTC GCC CTG TTG CCC TTC TCC CTC CCG CTC CTG GGC Pro Phe Lys Asn Leu Ala Leu Pro Phe Ser Leu Pro Leu Leu Gly	144
35 40 45	
GGA GGC GGA AGC GGA AGT GGC GAG AAA GTG TCG GTC TCC AAG ATG GCG Gly Gly Ser Gly Ser Gly Glu Lys Val Ser Val Ser Lys Met Ala	192
50 55 60	
GCC GCC TGG CCG TCT GGT CCG TCT GCT CCG GAG GCC GTG ACG GCC AGA Ala Ala Trp Pro Ser Gly Pro Ser Ala Pro Glu Ala Val Thr Ala Arg	240
65 70 75 80	
CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT ACA GGA CCC TGG GGG Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro Trp Gly	288
85 90 95	
GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG CTT AAG TGC GAG GAC Ala Val Ala Thr Ser Ala Gly Gly Glu Ser Leu Lys Cys Glu Asp	336
100 105 110	
CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA AAA ATA AAT GAC GCT Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn Asp Ala	384
115 120 125	
ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA GCT CAT GTT TCC TGT Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val Ser Cys	432
130 135 140	
TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT TCC AGT GGC AAT GAA ACA Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn Glu Thr	480
145 150 155 160	
CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG CCC ATA TCT TGC CGA His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser Cys Arg	528
165 170 175	
AAT GTA AAT GGC TAT TCC TAC AAA GTG GCA GTC GCA TTG TCT CTT TTT Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser Leu Phe	576
180 185 190	
CTT GGA TGG TTG GGA GCA GAT CGA TTT TAC CTT GGA TAC CCT GCT TTG Leu Gly Trp Leu Gly Ala Asp Arg Phe Tyr Leu Gly Tyr Pro Ala Leu	624
195 200 205	
GGT TTG TTA AAG TTT TGC ACT GTA GGG TTT TGT GGA ATT GGG AGC CTA Gly Leu Leu Lys Phe Cys Thr Val Gly Phe Cys Gly Ile Gly Ser Leu	672
210 215 220	
ATT GAT TTC ATT CTT ATT TCA ATG CAG ATT GTT GGA CCT TCA GAT GGA	720

Ile Asp Phe Ile Leu Ile Ser Met Gln Ile Val Gly Pro Ser Asp Gly
 225 230 235 240

AGT AGT TAC ATT ATA GAT TAC TAT GGA ACC AGA CTT ACA AGA CTG AGT
 Ser Ser Tyr Ile Ile Asp Tyr Tyr Gly Thr Arg Leu Thr Arg Leu Ser
 245 250 255

ATT ACT AAT GAA ACA TTT AGA AAA ACG CAA TTA TAT CCA TAA
 Ile Thr Asn Glu Thr Phe Arg Lys Thr Gln Leu Tyr Pro
 260 265

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Ile Leu Lys Gly Ser Pro Asn Val Ile Pro Arg Ala His Gly
 1 5 10 15

Gln Lys Asn Thr Arg Arg Asp Gly Thr Gly Leu Tyr Pro Met Arg Gly
 20 25 30

Pro Phe Lys Asn Leu Ala Leu Pro Phe Ser Leu Pro Leu Leu Gly
 35 40 45

Gly Gly Gly Ser Gly Ser Gly Glu Lys Val Ser Val Ser Lys Met Ala
 50 55 60

Ala Ala Trp Pro Ser Gly Pro Ser Ala Pro Glu Ala Val Thr Ala Arg
 65 70 75 80

Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro Trp Gly
 85 90 95

Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys Glu Asp
 100 105 110

Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn Asp Ala
 115 120 125

Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val Ser Cys
 130 135 140

Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn Glu Thr
 145 150 155 160

His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser Cys Arg
 165 170 175

Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser Leu Phe
 180 185 190

Leu Gly Trp Leu Gly Ala Asp Arg Phe Tyr Leu Gly Tyr Pro Ala Leu
195 200 205

Gly Leu Leu Lys Phe Cys Thr Val Gly Phe Cys Gly Ile Gly Ser Leu
210 215 220

Ile Asp Phe Ile Leu Ile Ser Met Gln Ile Val Gly Pro Ser Asp Gly
225 230 235 240

Ser Ser Tyr Ile Ile Asp Tyr Tyr Gly Thr Arg Leu Thr Arg Leu Ser
245 250 255

Ile Thr Asn Glu Thr Phe Arg Lys Thr Gln Leu Tyr Pro
260 265

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Met His Ile Leu Lys Gly Ser Pro Asn Val Ile Pro Arg Ala His Gly
1 5 10 15

48

CAG AAG AAC ACG CGA AGA GAC GGA ACT GGC CTC TAT CCT ATG CGA GGT

96

Gln	Lys	Asn	Thr	Arg	Arg	Asp	Gly	Thr	Gly	Leu	Tyr	Pro	Met	Arg	Gly		
			20					25					30				
CCC	TTT	AAG	AAC	CTC	GCC	CTG	TTG	CCC	TTC	TCC	CTC	CCG	CTC	CTG	GGC	144	
Pro	Phe	Lys	Asn	Leu	Ala	Leu	Leu	Pro	Phe	Ser	Leu	Pro	Leu	Leu	Gly		
			35					40					45				
GGA	GGC	GGA	AGC	GGA	AGT	GGC	GAG	AAA	GTG	TCG	GTC	TCC	AAG	ATG	GCG	192	
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Glu	Lys	Val	Ser	Val	Ser	Lys	Met	Ala		
			50				55					60					
GCC	GCC	TGG	CCG	TCT	GGT	CCG	TCT	GCT	CCG	GAG	GCC	GTG	ACG	GCC	AGA	240	
Ala	Ala	Trp	Pro	Ser	Gly	Pro	Ser	Ala	Pro	Glu	Ala	Val	Thr	Ala	Arg		
			65				70				75			80			
CTC	GTT	GGT	GTC	CTG	TGG	TTC	GTC	TCA	GTC	ACT	ACA	GGA	CCC	TGG	GGG	288	
Leu	Val	Gly	Val	Leu	Trp	Phe	Val	Ser	Val	Thr	Thr	Gly	Pro	Trp	Gly		
			85				90					95					
GCT	GTT	GCC	ACC	TCC	GCC	GGG	GGC	GAG	GAG	TCG	CTT	AAG	TGC	GAG	GAC	336	
Ala	Val	Ala	Thr	Ser	Ala	Gly	Gly	Glu	Glu	Ser	Leu	Lys	Cys	Glu	Asp		
			100				105					110					
CTC	AAA	GTG	GGA	CAA	TAT	ATT	TGT	AAA	GAT	CCA	AAA	ATA	AAT	GAC	GCT	384	
Leu	Lys	Val	Gly	Gln	Tyr	Ile	Cys	Lys	Asp	Pro	Lys	Ile	Asn	Asp	Ala		
			115				120					125					
ACG	CAA	GAA	CCA	GTT	AAC	TGT	ACA	AAC	TAC	ACA	GCT	CAT	GTT	TCC	TGT	432	
Thr	Gln	Glu	Pro	Val	Asn	Cys	Thr	Asn	Tyr	Thr	Ala	His	Val	Ser	Cys		
			130				135				140						
TTT	CCA	GCA	CCC	AAC	ATA	ACT	TGT	AAG	GAT	TCC	AGT	GGC	AAT	GAA	ACA	480	
Phe	Pro	Ala	Pro	Asn	Ile	Thr	Cys	Lys	Asp	Ser	Ser	Gly	Asn	Glu	Thr		
			145				150				155			160			
CAT	TTT	ACT	GGG	AAC	GAA	GTT	GGT	TTT	TTC	AAG	CCC	ATA	TCT	TGC	CGA	528	
His	Phe	Thr	Gly	Asn	Glu	Val	Gly	Phe	Phe	Lys	Pro	Ile	Ser	Cys	Arg		
			165				170				175						
AAT	GTA	AAT	GGC	TAT	TCC	TAC	AAA	GTG	GCA	GTC	GCA	TTG	TCT	CTT	TTT	576	
Asn	Val	Asn	Gly	Tyr	Ser	Tyr	Lys	Val	Ala	Val	Ala	Leu	Ser	Leu	Phe		
			180				185					190					
CTT	GGA	TGG	TTG	GGA	GCA	GAT	CGA	TTT	TAC	CTT	GGA	TAC	CCT	GCT	TTG	624	
Leu	Gly	Trp	Leu	Gly	Ala	Asp	Arg	Phe	Tyr	Leu	Gly	Tyr	Pro	Ala	Leu		
			195				200				205						
GGT	TTG	TTA	AAG	TTT	TGC	ACT	GTA	GGG	TTT	TGT	GGA	ATT	GGG	AGC	CTA	672	
Gly	Leu	Leu	Lys	Phe	Cys	Thr	Val	Gly	Phe	Cys	Gly	Ile	Gly	Ser	Leu		
			210				215				220						
ATT	GAT	TTC	ATT	CTT	ATT	TCA	ATG	CAG	ATT	GTT	GGA	CCT	TCA	GAT	GGA	720	
Ile	Asp	Phe	Ile	Leu	Ile	Ser	Met	Gln	Ile	Val	Gly	Pro	Ser	Asp	Gly		
			225				230				235			240			
AGT	AGT	TAC	ATT	ATA	GAT	TAC	TAT	GGA	ACC	AGA	CTT	ACA	AGA	CTG	AGT	768	
Ser	Ser	Tyr	Ile	Ile	Asp	Tyr	Tyr	Gly	Thr	Arg	Leu	Thr	Arg	Leu	Ser		
			245				250				255						
ATT	ACT	AAT	GAA	ACA	TTT	AGA	AAA	ACG	CAA	TTA	TAT	CCA	TAA			810	
Ile	Thr	Asn	Glu	Thr	Phe	Arg	Lys	Thr	Gln	Leu	Tyr	Pro					
			260				265										

(2) INFORMATION FOR SEQ ID NO:2:

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Gln Lys Asn Thr Arg Arg Asp Gly Thr Gly Leu Tyr Pro Met Arg Gly
20 25 30

Pro Phe Lys Asn Leu Ala Leu Pro Phe Ser Leu Pro Leu Leu Gly
35 40 45

Gly Gly Gly Ser Gly Ser Gly Glu Lys Val Ser Val Ser Lys Met Ala
50 55 60

Ala Ala Trp Pro Ser Gly Pro Ser Ala Pro Glu Ala Val Thr Ala Arg
65 70 75 80

Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro Trp Gly
85 90 95

Ala Val Ala Thr Ser Ala Gly Gly Glu Ser Leu Lys Cys Glu Asp
100 105 110

Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn Asp Ala
115 120 125

Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val Ser Cys
130 135 140

Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn Glu Thr
145 150 155 160

His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser Cys Arg
165 170 175

Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser Leu Phe
180 185 190

Leu Gly Trp Leu Gly Ala Asp Arg Phe Tyr Leu Gly Tyr Pro Ala Leu
195 200 205

Gly Leu Leu Lys Phe Cys Thr Val Gly Phe Cys Gly Ile Gly Ser Leu
210 215 220

Ile Asp Phe Ile Leu Ile Ser Met Gln Ile Val Gly Pro Ser Asp Gly
225 230 235 240

Ser Ser Tyr Ile Ile Asp Tyr Tyr Gly Thr Arg Leu Thr Arg Leu Ser
245 250 255

Ile Thr Asn Glu Thr Phe Arg Lys Thr Gln Leu Tyr Pro
260 265